

FIGURE 150

GCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCTGGCTATGTTAAACTCCAATGTCCTCTGTG
 GTTAACGTCTCTTGGCCATCAAGTTCAACCTCATTTGACAGCCCAAGCAGTATCCAGTTGTCAACAATAATATGG
 CAAAATCCGGGCGCTAAGAACACCGTTACCCATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTTA
 TGCCTCACCCCGCTCTGGAGAGAGCGGTTTCAGCCCCAGAACCCCGTCTCTGAGACTGGCATCCGAAATAC
 TACTCAGTTTGGCTCTGTGCTGGCCCGCCAGCACTGGATGAGAGATCCTTACTGTCATGACATCTGTCGCCCATCTGGTT
 TACCGCCATTTGGATACCTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCGCTTTACTTAAACATCTACGT
 GCCCAGCGAAGATGGAGCCCAACAAAGAAAACGCGAGATGATATAACGAGTAAATGACCCTGGTGAAGACGAAGA
 TATTCTATGATCAGAACAGTAAGAAGCCGCTCATGTTCTATATCCATGGGGGATCTTACATGGAGGGCAACGGGCAA
 CATGATTGACGCGACATTTTGGCAAGCTACGGAAACGTATCGTGATCACCATTAACCTACCCCTTGGGAATACT
 AGGGTTTTTAAAGTACCGGTGACACAGGCGACAAAGGCAACTATGGGCTCTGGATCAGATTCAAGCACTGGCGGTG
 GATTGAGGAGAATGTGGAGCCCTTTGGCGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCCTC
 CTGTGTGACGCTGTGACCCCTGTCCCACTACTCAGAAGGTCCTTCCAGAAGGCCATCATTAGAGCGGCGACCGC
 CCTGTCCAGCTGGGCGAGTGAACCTACAGCCGCGCCAAGTACACTCGSATATTGGCAGACAAGGTCTGGCTGCAACAT
 GCTGGACAACACGGACATGGTGAATGCTCGGGGAACAAAGACTACAAGGAGCTCATCCAGCAGACCATCACCCC
 GGCCACCTACCAATAGCCTTCGGGCGGTGATCGACGGCGACGTCATCCAGACAGCCCCAGATCCTGTATGGA
 GCAAGGCGAGTTCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCTGAAGTTCGTGGACGGCAT
 CGTGGATAACGAGGACGTTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAATCTCGTGGACAACCTTTACGG
 CTACCTCGAAGGGAAGACACTTTGCGGGAGACTCAAGTTTCACTGTACACAGACTGGGCGGATAGGAGAAAACCC
 GGAGACGCGCGGGAAGCCCTGGTGGCTCTCTTTACTGACCAAGTGGGTGGCCCGCGCGTGGGCCCGGACCT
 GCACGCGCAGTACGGCTCCCGCACTACTTCTATGCTTCTATCATCTGCGCAAAGGGAATGAAGCGCCGACTG
 GGCAGATTTCGGCCATGTGTGATGAGGTCCCTATGTCTTCGGCATCCCAATGATCGGTCCCAACGAGCTCTTCAG
 TTGTAACCTTTTCCAAAGACGAGCTCATGCTCAGCGCGTGGTCTGACCTCTGGAAGCACTTCGCCAAACCTGG
 TGTATCCAAATCAACAGTTCTCTCAGGATACCAAGTTCACTACACAAACCCAGCCGTTTGAAGAGATGCGCTG
 GTCCAAGTATAATCCAAAGACAGCTCTATCTGCATATGGCTTGAACACAGAGTGAAGAGATCTACTACCGGGC
 AAGCAAGTGGCTTTCTGGTTGGAATCTGTTCTCATTTGCACTATGCAACAGTATCCAGTATGTTTCAAC
 AACCACAAAGTTCCTCCACCAAGATGACATCATTTCCATGCGCACCCGGGATCTCCCGCAAGATATGGCC
 AACCCAAAGCGCCCAACATCACTCTGCAACAACTCCCAACACTCAAGACCTCAAGACCTCAACAAACGCGCGCTG
 GGACCAACTCTCTCATTAAGTAAACAAACAGAGATTATTCACCGAATTAAGTGTCAACATTGCCGTCCGGCGCTG
 GACTTTAAGACAAAATGCAAAAAGGCACTCATCCATCCCGGACAGCTTATGACGCCAAACCATCACCATGATTCAAA
 GAGCAGTCTGAAACAGATCACGAGTGTGAGTCTGTCGAGGACACGACACTGAGGCTCAGCTGCCCGCCAGA
 CTACACCTCTACGCTCGCCGCTCGCCAGATGACATCCCACTTATGACGCCAAACCATCACCATGATTCAAA
 CACACTGACGGGATCAGCCCTTTGCACACTTTTAAACCTTCAGTGGAGGACAAACAGTACAAATTTACCCCA
 CGGACATTTCCACCACTACAGTATAGCTTTTGGCCCTATTTCCCTTCTATCCCTCTGCTCCCTACCCGCTCAGCAACAT
 AGAAGAGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAGAAAGTCTCCAGACAGGAATGTTTGTGCCACT
 GACTTTAAGACAAAATGCAAAAAGGCACTCATCCATCCCGGACAGCTTATGACGCCAAACCATCACCATGATTCAAA
 AAGATCAACTCTGACCCCTGTGAAATGTGAGAAGTACACATTTCTGTTTAAATTAACCTGCTTTAAGATCTTACCA
 CTCCATCAATGTTTGTGTGATAGGACATCACATTTCAAGGCCCGGGTGTTCACACGCTATGGAAGACAGCT
 GACACTTCTGAAACTCAGCCAAAGGACACTTGATATTTTAAATTAACATGGAAGTTTAAACATTTCTTTCTGTGTC
 CACACAAATGGATGGCTCTCTTTAAGTGAAGAAAGAGTCAATGAGATTTTCCAGCAGCATGGAGCTGTAATCCAG
 AGAAGAAAGAACTAGAAATTTATTTATTAAGAAATGGACTGTGCGAGCAAACTGTACGGTCTGTGTCAAAGAG
 GTGTTTTCGACGCTGAACATATTTAAGAGACTTTGT

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FIGURE 151

MLNSNVLLWLTAIAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP
PTGERRFQPPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN
EDCLYLNIVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGLFSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDPDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVVYV
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNPVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDITVLIETKRDYSTELSVTI AVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSQQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCTCPDYLTLRLRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

0973235.101501

FIGURE 152

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAACGGGAGCACTCGCTCGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG
GTGCCATGTTTCTCGAGAGACTGGGAGTTGCAGGTGCACCTTCAAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTCGTGTGATTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCCGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCTTGAAGTTGTTTGAACCTGACAGTGGAGAGAACCOCAGAAAGGAAAAAGCTCCATCGA
TAGTGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCCTGGCCCTTCTCCTCATCGTCTTTTCTCCCTGGTGTCTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACTTTTGTGACTGTACCCCATGAGGTATGGAAGGAGCAGGCACCTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTGGGGACATATTTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTTCCATGGTTGTGCATGGGACATCTAATC
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGTGCTGTGTATGTGCCTTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC
AGAATTTCATAGCCAGGCTGCCGTGTTGTTTGAAGTGCAGAGGCCCTTCTACTTCAGTTTTG
AATCCACAAGAATTAATAACTGGTAACACCACAGGCTTTCTGACCATCCATTCTGTTGGGTT
TTGCATTTGACCCAAACCTCTGCCTACCTGAGGAGCTTTCTTGGAAACAGGATGGAAACT
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTCAATTGCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCTGGGGCTGCAGAACACACCTGCGTTTCA
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCTGGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAAACCAAAGCAACATTTGTGATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTGTGCTAGAGCCTGCTTAGCTGCATGTTTGTAGT
TACGATTTTTTGAATCCCACTTTGAGTGTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCCAGAGAAGAAATTTGGCTTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTTTCTCATGTTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCTGGTGGAAAGATT
CACTGTCAATTGAGCAGCAGCCTGAGTGTGCGCTCTGTCAACCCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCGCTGGGATTAAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCTGGAACTCTGAGTCTCTTATGAACCTCTGTGAGCCTAAATGAAAT
TCTTAAATCACCAGATGGAACCAAAAAAAAAAAAAAAAAAGGGCGCCGCGACTCTAGAGTGC
ACCTGCAGTAGGATAACAGGTAATAAGCTTGGCCCGCATGG

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